CLAIMS

1. A set of nucleic acid segments for identifying the CCR5 haplotype group of both alleles of a human subject, which set comprises at least one nucleic acid segment capable of detecting each of the following haplotype groups, each haplogroup being defined in terms of the nucleotides at positions 29, 208, 303, 627, 630, 676 and 927 of the human CCR5 sequence as shown in SEQ.ID.NO.:65, with definition of the amino acid at position 64 and the presence or absence of the Δ32 deletion, as follows:

Haplogroup	Nucleotide position in CCR5 sequence 29 208 303 627 730 676 927	
HHA:	A G G T C A C	
HHB:	A T G T C A C	
HHC:	A T G T C G C	
HHD:	A T G T T A C	
HHE:	A G A C C A C	
HHF*1:	A G A C C A T	
HHF*2:	A G A C C A T	isoleucine at amino acid 64
HHG*1:	G G A C C A C	
HHG*2:	G G A C C A C	has Δ32, 32 base pair deletion

2. A set of nucleic acid segments for identifying the CCR5 haplotype group of both alleles of a human subject, which set comprises at least one nucleic acid segment capable of detecting each of the human haplotype groups described in the phylogenetic tree set out in Figure 1B.

3. A set of nucleic acid segments as claimed in claim 1 or claim 2, which further comprises at least one nucleic acid segment capable of detecting a human CCR2 polymorphism at both alleles.

4. A set of nucleic acid segments as claimed in claim 3, which comprises at least a first and a second nucleic acid segment that is each capable of detecting a distinct human CCR2 polymorphism at both alleles.

5. A set of nucleic acid segments as claimed in any one of claims 1 to 4, each segment being a primer.

6. A nucleic acid segment for identifying a CCR5 haplotype group of a human subject, which nucleic acid segment is capable of detecting the human haplotype group HHD, which has nucleotide A at position 29, T at position 208, G at position 303, T at position 627, T at position 630, A at position 676 and C at position 927 of the human CCR5 sequence as shown in SEQ.ID.NO.:65.

7. A set of nucleic acid segments for identifying the CCR5 haplotype group of both alleles of a human subject, which set comprises a nucleic acid segment as claimed in claim 6.

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8. A set of nucleic acid segments as clamed in claim 7, wherein each nucleic acid segment is a primer.

9. A kit comprising a set of nucleic acid segments as claimed in any one of claims 1 to 5, 7 and 8, or a nucleic acid segment as claimed in claim 6, and further components for carrying out the identification of the CCR5 haplogroup(s).

10. A kit comprising a set of nucleic acid segments as claimed in any one of claims 1 to 5, 7 and 8, or a nucleic acid segment as claimed in claim 6, further comprising instructions for identifying the CCR5 haplotype group of both alleles of a human subject and for correlating the haplogroups on both CCR5 alleles with the risk of HIV-1 infection or disease progression in humans, and which optionally further comprises further components for carrying out the identification of the CCR5 haplogroup(s).

11. A kit as claimed in claim 9 or claim 10, wherein the kit comprises a restriction endonuclease.

12. A method which comprises identifying the CCR5 haplotype group of both alleles of a human subject using a set of nucleic acid segments as claimed in any one of claims 1 to 5, 7 and 8, or a nucleic acid segment as claimed in claim 6.

13. A method comprising identifying the CCR5 haplotype group of both alleles of each member of a cohort of human subjects of a chosen population, the human CCR5 haplotype groups being as defined in claim 1 or as described in Figure 1B, and determining the correlation of the pairs of haplotype groups with risk of HIV-1 infection, transmission or disease progression in that population.

14. A method as claimed in claim 13, wherein the population is an ethnic group.

15. A method as claimed in claim 13 or claim 14, wherein the population is children.

16. A method as claimed in any one of claims 13 to 15, wherein human CCR2 polymorphisms at both alleles are also identified and correlated with risk of HIV-1 infection, transmission or disease progression in that population.

17. A method of assessing the risk of a human subject for HIV-1 infection, transmission or disease progression, comprising identifying the CCR5 haplotype group of both alleles of the human subject using a set of nucleic acid segments as claimed in any one of claims 1 to 5, 7 and 8, or a nucleic acid segment as claimed in claim 6, and correlating the pair of haplogroups identified with the risk of HIV-1 infection, transmission or disease progression associated with that pair of haplogroups.

18. A method as claimed in claim 17, wherein the pair of haplogroups identified for the human subject is correlated with the risk of HIV-1 infection, transmission or disease

progression associated with that pair of haplogroups for a population to which the subject belongs.

19. A method as claimed in claim 18, wherein the correlation between haplogroup pairs and risk of HIV-1 infection, transmission or disease progression has been determined as claimed in any one of claims 13 to 16.

20. A method as claimed in claim 18, wherein the human subject is Caucasian and the presence of two HHE alleles as defined in claim 1 is indicative of an increased risk of HIV-1 infection or disease progression.

21. A method as claimed in claim 18, wherein the human subject is African-American and the presence of an HHC and an HHF*1 haplogroup, an HHC and an HHE haplogroup, two HHC haplogroups, or an HHC and an HHD haplogroup, the haplogroups being as defined in claim 1, is indicative of an increased risk of HIV-1 infection or disease progression.

22. A method as claimed in claim 18, wherein the human subject is a child and the presence of an HHC and an HHE haplogroup, two HHE haplogroups, or an HHE haplogroup and an HHG*2 haplogroup, the haplogroups being as defined in claim 1, is indicative of an increased risk of HIV-1 transmission, infection or disease progression.

23. A method of reducing HIV-1 infection, transmission or disease progression in a human subject comprising identifying a susceptible human subject by a method as claimed in any one of claims 17 to 22 and treating a susceptible human subject with a biologically effective amount of at least a first anti-viral agent.